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Om protein - protein search, using sw model

Run on: March 1, 2001, 16:09:02 ; search time 299.73 Seconds  
 (without alignments)  
 26.982 Million cell updates/sec

Title: US-09-331-631a-1\_COPY\_117\_185

perfect score: 384

Sequence: 1\_NQRDPROQYEQCQKHCQRR.....EBQQREDEEKYERMKEEDN 69

Scoring table: BLOSUM62

Gapp 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SPTREMBL\_15:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_minc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match Length	DB ID	Description
1	384	100.0	666	10_09SPL5	09SP15 macadamia i
2	367	95.6	666	10_09SPL5	09SP14 macadamia i
3	363	94.5	625	10_09SPL3	09SP13 macadamia i
4	172	44.8	525	10_043358	043358 theobroma c
5	163	42.4	593	10_09SEW4	09SEW4 juglans reg
6	120.5	31.4	554	5_Q9VPS3	Q9VPS3 drosophila
7	116.5	30.3	1038	5_060983	060983 dictyosteli
8	115	29.9	1089	5_060947	040947 kposi's sa
9	114	29.7	810	10_09ZWI3	Q9ZWI3 cucurbita m
10	107	27.9	1162	12_098148	Q98148 kaposi's sa
11	105.5	27.5	1129	12_09QR71	Q9Q71 kaposi's sa
12	105	27.3	1737	5_Q9Tw28	Q9Tw28 dictyosteli
13	104.5	27.2	385	5_017909	Q17909 caenorhabdi
14	104	27.1	1390	5_077033	077033 dictyosteli
15	103	26.8	838	5_Q9YOC9	Q9YOC9 dictyosteli
16	101	26.3	233	4_Q9UF22	Q9UF22 homo sapien
17	101	26.3	289	4_Q9NU6	Q9NU6 homo sapien
18	101	26.3	1027	4_Q9NST7	Q9NST7 homo sapien
19	101	26.3	1165	4_095819	095819 homo sapien

**ALIGMENTS**

RESULT	1
09SPL5	PRELIMINARY;
ID 09SPL5;	PRT; 666 AA.
AC 09SPL5;	
DT 01-MAY-2000 (TRIMBLErel. 13, Last sequence update)	
DT 01-OCT-2000 (TRIMBLErel. 15, Last annotation update)	
DE VICTILIN PRECURSOR.	
GN AMP2.	
OS Macadamia integrifolia (Macadamia nut).	
OC Eukaryota; Viriplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
OX NCBI_TaxID=6098;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=NUT KERNEL;	
RA Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;	"A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia kernels."	
RT Plant J. 0:0-0(1999).	
DR EMBL; AF161883; AAD54244.1; -.	
DR HSSP; P02853; 2BHL.	
DR INTERPRO; IPR00113; -.	
DR PFAM; PF00546; Seedstore_7s; 1_C75BDB884B2DF0224 CRC64;	
SQ SEQUENCE 666 AA; 78217 MW;	
Query Match Best Local Similarity 100.0%; Score 384; DB 10; Length 666; Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1_NQRDPROQYEQCQKICORRETEPRIMOTCOQCRCERYKEKKQOKRYBQOREDEEKY 60	
Db 117_NQRDPROQYEQCQKICORRETEPRIMOTCOQCRCERYKEKKQOKRYBQOREDEEKY 176	
QY 61_ERMKEEDN 69	
Db 177_ERMKEEDN 185	
RESULT 2	
09SPL4	

QY	61	EERMKEEDN	59	
AC	09SP34	PRELIMINARY;	PRT;	666 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	VICILIN PRECURSOR.			
GN	AMP2.			
OS	Macadamia integrifolia (Macadamia nut).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.			
OX	NCBI_TAXID=60698;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=NUT KERNEL;			
RA	Marcus J.P.; Goultier K.C.; Green J.L.; Manners J.M.;			
RT	"A family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia.";			
RT	Plant J. 0:0-0 (1999).			
RL	0:0-0 (1999).			
DR	EMBL; AF161884; AAD54245.1; -.			
DR	HSSP; P02853; 2PHL.			
DR	INTERPRO; IPR001113; -.			
DR	PFAM; PF00546; Seedstore_7s; 1.			
SQ	SEQUENCE 666 AA; 70243 MW; 0ECA22F8710F8A7B CRC64;			
RESULT	4			
Q9SP33	PRELIMINARY; PRM; 625 AA.			
ID	043358	PRELIMINARY;	PRT;	525 AA.
AC	043358;			
DT	043358;			
DT	01-NOV-1995 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	VICILIN PRECURSOR.			
GN	[1]			
RC	SEQUENCE FROM N.A.			
RA	Theobroma cacao (Cacao).			
RT	"Comparison of the structure and nucleotide sequences of vicilin genes of cocoa and cotton raise questions about vicilin evolution.";			
RT	Plant Mol. Biol. 18:1173-1176 (1992).			
RL	McHenry L.; Fritz P.J.;			
DR	EMBL; X62625; CAA4493.1; -.			
DR	X62626; CAA4494.1; -.			
DR	HSSP; P02833; 2PHL.			
DR	INTERPRO; IPR001113; -.			
DR	PFAM; PF00546; Seedstore_7s; 1.			
DR	PRODOM; PD08105; -; 1.			
KW	Signal.			
FT	SIGNAL 1 24 POTENTIAL.			
SQ	SEQUENCE 525 AA; 60798 MW; 19114CD5C248905D CRC64;			
RESULT	3			
Q9SP33	PRELIMINARY; PRM; 625 AA.			
ID	043358	PRELIMINARY;	PRT;	525 AA.
AC	043358;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DE	VICILIN PRECURSOR (FRAGMENT).			
GN	AMP2.			
OS	Macadamia integrifolia (Macadamia nut).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.			
OX	NCBI_TAXID=60698;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Marcus J.P.; Goultier K.C.; Green J.L.; Manners J.M.;			
RT	"A family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia.";			
RT	Plant J. 0:0-0 (1999).			
DR	EMBL; AF161885; AAD54246.1; -.			
DR	HSSP; P02853; 2PHL.			
DR	INTERPRO; IPR001113; -.			
DR	PFAM; PF00546; Seedstore_7s; 1.			
SQ	SEQUENCE 625 AA; 73586 MW; 415808A89D370296 CRC64;			
RESULT	5			
Q9SEW4	PRELIMINARY; PRT; 593 AA.			
ID	043358	PRELIMINARY;	PRT;	593 AA.
AC	043358;			
DT	043358;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).			
OS	Juglans regia (English walnut).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;			
OC	Fagales; Juglandaceae; Juglans.			
OX	NCBI_TAXID=51240;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV_SUNLAND; TISSUE=SOMATIC EMBRYO LINE;			
RA	Teuber S.S.; Jarvis K.C.; Peterson W.R.; Dandekar A.M.; Ansari A.A.;			
RT	"Identification and cloning of a cDNA encoding a vicilin-like protein, Jug r 2, from English walnut kernel (Juglans regia): a major food			
RT	protein."			







RESULT 14  
077033  
ID 077033  
PC 077033 PRELIMINARY; PRT; 1390 AA.

Search completed: March 1, 2001, 16:09:05  
Job time: 1549 sec

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DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TRFA.
GN Dicystostelium discoideum (Slime mold).
OS Eukaryota; Dictyosteliida; Dictyostelium.
OC NCBI-TaxID=41689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A22;
RA Saito J., Adachi H., Sutoh K. ;
RT "Dictyostelium TRFA homologous to yeast Ssn6 is required for normal
growth and early development";
RL J. Biol. Chem. 0:0-0(1998);
EMBL:AB009080; BAA3343.1; -.
DR IPR01440; -.
PFAM:PF00515; TPR; 9.
DR SEQUENCE 1390 AA; 160421 MW; BAAAB9926656002DE CRC64;

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query Match 27.1%; Score 104; DB 5; Length 1390;  
 Best Local Similarity 23.9%; Pred. NO: 0.075; S0: 0.075;  
 Matches 16; Conservative 0; Mismatches 21; Indels 0; Gaps 0

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ID OX90C9; PRELIMINARY; PRT; 838 AA.
AC Q9IVOC9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE RAS INTERACTING PROTEIN RIPA.
GN RIPA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryote; Dictyosteliida; Dictyostelium.
OX NCBI_TAXID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee S., Parent C.A., Insaal R., Firsel R.A.:
RT "The novel ras interacting protein required for chemotaxis and cAMP
signal relay in Dictyostelium."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF115241; AAC43567.1;
SEQUENCE 838 AA: 94059 MW: EAAD91294226808 CRC64;
SQ

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Query Match 26.8%; Score 103; DB 5; Length 838;  
 Best Local Similarity 23.9%; Prcd. No. 0.061; Mismatches 33; Matches 16; Conservative 18; Indels 0; Gaps 0